Recombinant SARS-CoV-2 B.1.620 Spike RBD His-tag

Catalog Number: 10907-CV

DESCRIPTION

Source	Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike RBD protein Arg319-Phe541 (Ser477Asn, Glu484Lys), with a C-terminal His tag Accession # YP_009724390.1
N-terminal Sequence Analysis	Arg319
Predicted Molecular Mass	26 kDa

SPECIFICATIONS

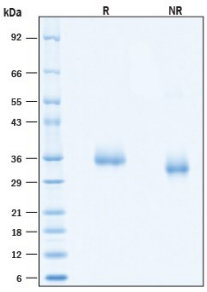
SDS-PAGE	32-38 kDa, under reducing conditions
Activity	Measured by its binding ability in a functional ELISA with Recombinant Human ACE-2 His-tag (Catalog # 933-ZN).
Endotoxin Level	<0.10 EU per 1 µg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and quantitative densitometry by Coomassie® Blue Staining.
Formulation	Lyophilized from a 0.2 µm filtered solution in PBS with Trehalose. See Certificate of Analysis for details.

PREPARATION AND STORAGE

Reconstitution	Reconstitute at 500 µg/mL in PBS.
Shipping	The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	**Use a manual defrost freezer and avoid repeated freeze-thaw cycles.** • 12 months from date of receipt, -20 to -70 °C as supplied. • 1 month, 2 to 8 °C under sterile conditions after reconstitution. • 3 months, -20 to -70 °C under sterile conditions after reconstitution.

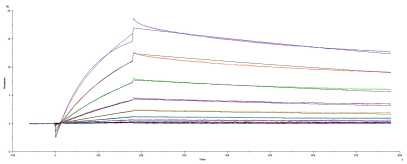
DATA

SDS-PAGE



Recombinant SARS-CoV-2 B.1.620 Spike RBD His-tag Protein SDS-PAGE. 2 µg/lane of Recombinant SARS-CoV-2 B.1.620 Spike RBD His-tag (Catalog # 10907-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 32-38 kDa.

Surface Plasmon Resonance (SPR)



Binding of ACE-2 to SARS-CoV-2 B.1.620 variant Spike RBD protein by surface plasmon resonance (SPR). Recombinant SARS-CoV-2 B.1.620 variant Spike RBD protein His-tag (Catalog #10907-CV) was immobilized on a Biacore Sensor Chip CM5, and binding to recombinant human ACE-2 (Catalog # 933-ZN) was measured at a concentration range between 0.184 nM and 94.3 nM. The double-referenced sensorgram was fit to a 1:1 binding model to determine the binding kinetics and affinity, with an affinity constant of K_D=4.40 nM.

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BACKGROUND

SARS-CoV-2, which causes the global pandemic coronavirus disease 2019 (Covid-19), belongs to a family of viruses known as coronaviruses that also include MERS and SARS-CoV-1. Coronaviruses are commonly comprised of four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M) and Nucleocapsid protein (N) (1). The SARS-CoV-2 S protein is a glycoprotein that mediates membrane fusion and viral entry. The S protein is homotrimeric, with each ~180-kDa monomer consisting of two subunits, S1 and S2 (2). In SARS-CoV-2, as with most coronaviruses, proteolytic cleavage of the S protein into S1 and S2 subunits is required for activation. The S1 subunit is focused on attachment of the protein to the host receptor while the S2 subunit is involved with cell fusion (3-5). A metallopeptidase, angiotensin-converting enzyme 2 (ACE2), has been identified as a functional receptor for SARS-CoV-2 through interaction with a receptor binding domain (RBD) located at the C-terminus of S1 subunit (6,7). The RBD of SARS-CoV-2 shares 73% amino acid (aa) identity with the RBD of the SARS-CoV-1, but only 22% aa identity with the RBD of MERS. A SARS-CoV-2 variant (B.1.620) carrying the aa substitution Ser477Asn and Glu484Lys in the RBD was first identified in Lithuania and quickly spread to other European countries and central Africa (8). Whether these mutations in the RBD would cause more severe symptom or decrease the efficacy of vaccine-induced immunity is still under investigation.

References:

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